

ABSTRACT

An apparatus, system and method for predicting single nucleotide polymorphisms (SNPs) is disclosed. The present invention generally includes steps for obtaining a variation predictiveness matrix and predicting one or more single nucleotide variations of a nucleic acid sequence based on the variation predictiveness matrix. The variation predictiveness matrix may be made by calculating the variation frequency from a first base to a second base in a dataset of two or more bases and determining a variation predictiveness value from the calculated variation frequency.

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